

Sequence listing

<110> Kaneka Corporation

<120> Process for producing coenzyme Q10

<130> T549/QX-GT2

<150> JP P1999-237561

<151> 1999-08-24

<160> 2

<210> 1

<211> 1653

<212> DNA

<213> Saioella complicata

<400> 1

ttttgtgggg tcgaaaagtc ggcacgggtg cagggtcggc ttgagaccag taaaggctcg 60

gagattgagt tcaggacaaa gctttgatcc gtgaggtcta catcttcagc aaatcatttc 120

aaatccatat acc atg gcc tca cca gca ctg cgg ata cga agc atc agc 169

Met Ala Ser Pro Ala Leu Arg Ile Arg Ser Ile Ser

1

5

10

tct cga tca atc gcc tct ctg cga tcg gtt acc cta aga aca gcc tcg 217

Ser Arg Ser Ile Ala Ser Leu Arg Ser Val Thr Leu Arg Thr Ala Ser

15

20

25

gca cct tca tta cga cta aga tgt acc ccg acg agc cgg cca tcg agt 265

Ala Pro Ser Leu Arg Leu Arg Cys Thr Pro Thr Ser Arg Pro Ser Ser

30

35

40

tca tgg gct gct gct gtg tct tcg gcg tcg aga ctg gtt gag cct gat 313

Ser Trp Ala Ala Ala Val Ser Ser Ala Ser Arg Leu Val Glu Pro Asp

45

50

55

60

ccg aat caa cct ctc atc aat ccg ctc aac ttg gtc ggt ccc gag atg 361

Pro Asn Gln Pro Leu Ile Asn Pro Leu Asn Leu Val Gly Pro Glu Met

65

70

75

tca aat ctt aca tcc aac atc cga tct ctc ctc ggt tca gga cac cct 409

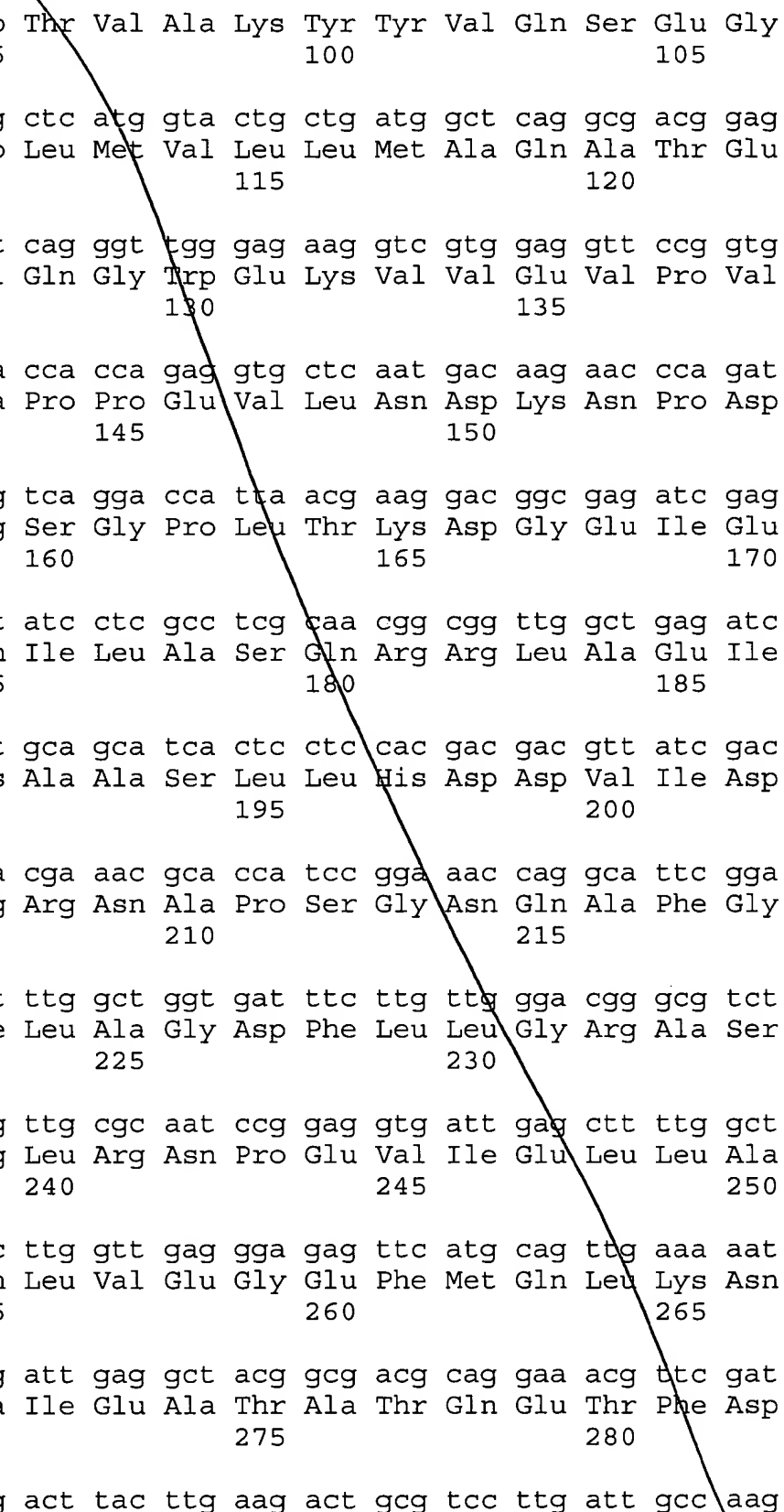
Ser Asn Leu Thr Ser Asn Ile Arg Ser Leu Leu Gly Ser Gly His Pro

80

85

90

tct ctc gac act gtc gct aaa tac tat gtt cag tct gag gga aag cat 457



Ser	Leu	Asp	Thr	Val	Ala	Lys	Tyr	Tyr	Val	Gln	Ser	Glu	Gly	Lys	His	
		95					100					105				
att	cgt	ccg	ctc	atg	gta	ctg	ctg	atg	gct	cag	gcg	acg	gag	gtt	gcg	505
Ile	Arg	Pro	Leu	Met	Val	Leu	Leu	Met	Ala	Gln	Ala	Thr	Glu	Val	Ala	
	110					115					120					
cca	aaa	gtt	cag	ggt	tgg	gag	aag	gtc	gtg	gag	gtt	ccg	gtg	aac	gag	553
Pro	Lys	Val	Gln	Gly	Trp	Glu	Lys	Val	Val	Glu	Val	Pro	Val	Asn	Glu	
125					130					135					140	
gga	ctc	gca	cca	cca	gag	gtg	ctc	aat	gac	aag	aac	cca	gat	atg	atg	601
Gly	Leu	Ala	Pro	Pro	Glu	Val	Leu	Asn	Asp	Lys	Asn	Pro	Asp	Met	Met	
				145					150					155		
aac	atg	agg	tca	gga	cca	tta	acg	aag	gac	ggc	gag	atc	gag	gga	cag	649
Asn	Met	Arg	Ser	Gly	Pro	Leu	Thr	Lys	Asp	Gly	Glu	Ile	Glu	Gly	Gln	
			160					165					170			
acg	tcg	aat	atc	ctc	gcc	tcg	caa	cgg	cgg	ttg	gct	gag	atc	acg	gag	697
Thr	Ser	Asn	Ile	Leu	Ala	Ser	Gln	Arg	Arg	Leu	Ala	Glu	Ile	Thr	Glu	
		175					180					185				
atg	atc	cat	gca	gca	tca	ctc	ctc	cac	gac	gac	gtt	atc	gac	gct	tcc	745
Met	Ile	His	Ala	Ala	Ser	Leu	Leu	His	Asp	Asp	Val	Ile	Asp	Ala	Ser	
	190					195					200					
gag	acc	aga	cga	aac	gca	cca	tcc	gga	aac	cag	gca	ttc	gga	aac	aag	793
Glu	Thr	Arg	Arg	Asn	Ala	Pro	Ser	Gly	Asn	Gln	Ala	Phe	Gly	Asn	Lys	
205					210					215					220	
atg	gcg	att	ttg	gct	ggt	gat	ttc	ttg	ttg	gga	cgg	gcg	tct	gtt	gca	841
Met	Ala	Ile	Leu	Ala	Gly	Asp	Phe	Leu	Leu	Gly	Arg	Ala	Ser	Val	Ala	
				225				230						235		
ttg	gcg	agg	ttg	cgc	aat	ccg	gag	gtg	att	gag	ctt	ttg	gct	act	gtt	889
Leu	Ala	Arg	Leu	Arg	Asn	Pro	Glu	Val	Ile	Glu	Leu	Leu	Ala	Thr	Val	
			240					245					250			
att	gca	aac	ttg	gtt	gag	gga	gag	ttc	atg	cag	ttg	aaa	aat	act	gtt	937
Ile	Ala	Asn	Leu	Val	Glu	Gly	Glu	Phe	Met	Gln	Leu	Lys	Asn	Thr	Val	
		255					260					265				
gat	gat	gcg	att	gag	gct	acg	gcg	acg	cag	gaa	acg	ttc	gat	tac	tat	985
Asp	Asp	Ala	Ile	Glu	Ala	Thr	Ala	Thr	Gln	Glu	Thr	Phe	Asp	Tyr	Tyr	
	270					275					280					
ttg	cag	aag	act	tac	ttg	aag	act	gcg	tcc	ttg	att	gcc	aag	tcg	tgc	1033

Leu Gln Lys Thr Tyr Leu Lys Thr Ala Ser Leu Ile Ala Lys Ser Cys
 285 290 295 300
 aga gca agt gcg ctt ctg ggt ggt gct acg cct gag gtt gct gat gct 1081
 Arg Ala Ser Ala Leu Leu Gly Gly Ala Thr Pro Glu Val Ala Asp Ala
 305 310 315
 gct tat gct tac gga agg aac ctt ggt ttg gca ttc cag atc gtc gac 1129
 Ala Tyr Ala Tyr Gly Arg Asn Leu Gly Leu Ala Phe Gln Ile Val Asp
 320 325 330
 gac atg ctc gac tac acc gtc tcc gct acc gac ctc ggt aag ccc gcc 1177
 Asp Met Leu Asp Tyr Thr Val Ser Ala Thr Asp Leu Gly Lys Pro Ala
 335 340 345
 ggt gca gac ctc cag ctc ggt ctc gcc acc gcg ccg gcc ctc ttc gca 1225
 Gly Ala Asp Leu Gln Leu Gly Leu Ala Thr Ala Pro Ala Leu Phe Ala
 350 355 360
 tgg aag cac cac gcc gag ctc ggt ccc atg atc aag cgc aag ttc tct 1273
 Trp Lys His His Ala Glu Leu Gly Pro Met Ile Lys Arg Lys Phe Ser
 365 370 375 380
 gac cca gga gac gtc gag cgt gca cgc gag ttg gtc gag aaa agt gat 1321
 Asp Pro Gly Asp Val Glu Arg Ala Arg Glu Leu Val Glu Lys Ser Asp
 385 390 395
 gga ttg gag aag acg aga gcc ttg gcg gag gag tat gcc cag aag gcg 1369
 Gly Leu Glu Lys Thr Arg Ala Leu Ala Glu Glu Tyr Ala Gln Lys Ala
 400 405 410
 ttg gat gca att cgg acg ttc ccg gag agt ccg gca cgg aag gct ttg 1417
 Leu Asp Ala Ile Arg Thr Phe Pro Glu Ser Pro Ala Arg Lys Ala Leu
 415 420 425
 gag cag ttg acg gac aag gtg ttg act agg tca aga taggaattcg agct 1467
 Glu Gln Leu Thr Asp Lys Val Leu Thr Arg Ser Arg
 430 435 440
 cggtacccgg ggatcctcta gagtcgacct gcaggcatgc aagcttggt gttttggcgg 1527
 atgagagaag attttcagcc tgatacagat taaatcagaa ccgagaagcg gtctgataaa 1587
 acagaatttg cctggcggca gtagcgcggt ggtccacact gaacctatgc cgaactcaga 1647
 agtgaa 1653

<210> 2

<211> 440

<212> PRT

<213> *Salicella complicata*

<400> 2

Met	Ala	Ser	Pro	Ala	Leu	Arg	Ile	Arg	Ser	Ile	Ser	Ser	Arg	Ser
1				5					10					15
Ile	Ala	Ser	Leu	Arg	Ser	Val	Thr	Leu	Arg	Thr	Ala	Ser	Ala	Pro
				20					25					30
Ser	Leu	Arg	Leu	Arg	Cys	Thr	Pro	Thr	Ser	Arg	Pro	Ser	Ser	Ser
				35					40					45
Trp	Ala	Ala	Ala	Val	Ser	Ser	Ala	Ser	Arg	Leu	Val	Glu	Pro	Asp
				50					55					60
Pro	Asn	Gln	Pro	Leu	Ile	Asn	Pro	Leu	Asn	Leu	Val	Gly	Pro	Glu
				65					70					75
Met	Ser	Asn	Leu	Thr	Ser	Asn	Ile	Arg	Ser	Leu	Leu	Gly	Ser	Gly
				80					85					90
His	Pro	Ser	Leu	Asp	Thr	Val	Ala	Lys	Tyr	Tyr	Val	Gln	Ser	Glu
				95					100					105
Gly	Lys	His	Ile	Arg	Pro	Leu	Met	Val	Leu	Leu	Met	Ala	Gln	Ala
				110					115					120
Thr	Glu	Val	Ala	Pro	Lys	Val	Gln	Gly	Trp	Glu	Lys	Val	Val	Glu
				125					130					135
Val	Pro	Val	Asn	Glu	Gly	Leu	Ala	Pro	Pro	Glu	Val	Leu	Asn	Asp
				140					145					150
Lys	Asn	Pro	Asp	Met	Met	Asn	Met	Arg	Ser	Gly	Pro	Leu	Thr	Lys
				155					160					165
Asp	Gly	Glu	Ile	Glu	Gly	Gln	Thr	Ser	Asn	Ile	Leu	Ala	Ser	Gln
				170					175					180
Arg	Arg	Leu	Ala	Glu	Ile	Thr	Glu	Met	Ile	His	Ala	Ala	Ser	Leu
				185					190					195
Leu	His	Asp	Asp	Val	Ile	Asp	Ala	Ser	Glu	Thr	Arg	Arg	Asn	Ala
				200					205					210
Pro	Ser	Gly	Asn	Gln	Ala	Phe	Gly	Asn	Lys	Met	Ala	Ile	Leu	Ala
				215					220					225
Gly	Asp	Phe	Leu	Leu	Gly	Arg	Ala	Ser	Val	Ala	Leu	Ala	Arg	Leu
				230					235					240
Arg	Asn	Pro	Glu	Val	Ile	Glu	Leu	Leu	Ala	Thr	Val	Ile	Ala	Asn
				245					250					255
Leu	Val	Glu	Gly	Glu	Phe	Met	Gln	Leu	Lys	Asn	Thr	Val	Asp	Asp
				260					265					270
Ala	Ile	Glu	Ala	Thr	Ala	Thr	Gln	Glu	Thr	Phe	Asp	Tyr	Tyr	Leu
				275					280					285
Gln	Lys	Thr	Tyr	Leu	Lys	Thr	Ala	Ser	Leu	Ile	Ala	Lys	Ser	Cys
				290					295					300
Arg	Ala	Ser	Ala	Leu	Leu	Gly	Gly	Ala	Thr	Pro	Glu	Val	Ala	Asp
				305					310					315

cont'd

Ala	Ala	Tyr	Ala	Tyr	Gly	Arg	Asn	Leu	Gly	Leu	Ala	Phe	Gln	Ile
				320					325					330
Val	Asp	Asp	Met	Leu	Asp	Tyr	Thr	Val	Ser	Ala	Thr	Asp	Leu	Gly
				335					340					345
Lys	Pro	Ala	Gly	Ala	Asp	Leu	Gln	Leu	Gly	Leu	Ala	Thr	Ala	Pro
				350					355					360
Ala	Leu	Phe	Ala	Trp	Lys	His	His	Ala	Glu	Leu	Gly	Pro	Met	Ile
				365					370					375
Lys	Arg	Lys	Phe	Ser	Asp	Pro	Gly	Asp	Val	Glu	Arg	Ala	Arg	Glu
				380					385					390
Leu	Val	Glu	Lys	Ser	Asp	Gly	Leu	Glu	Lys	Thr	Arg	Ala	Leu	Ala
				395					400					405
Glu	Glu	Tyr	Ala	Gln	Lys	Ala	Leu	Asp	Ala	Ile	Arg	Thr	Phe	Pro
				410					415					420
Glu	Ser	Pro	Ala	Arg	Lys	Ala	Leu	Glu	Gln	Leu	Thr	Asp	Lys	Val
				425					430					435
Leu	Thr	Arg	Ser	Arg										
				440										